

SEQUENCE LISTING

<110> Hjort, Carsten
Hondel, C.A.M.J.J. van den
Punt, P.J.
Shuren, F.H.J.
Christensen, Tove

<120> Fungal Transcriptional Activator Useful In Methods For Producing Polypeptides

<130> 5555.410-US

<160> 30

<170> PatentIn version 3.0

<210> 1
<211> 4098
<212> DNA
<213> Aspergillus niger

<220>
<221> exon
<222> (977) .. (1204)

<220>
<221> exon
<222> (1317) .. (1718)

<220>
<221> exon
<222> (1777) .. (2202)

<220>
<221> exon
<222> (2253) .. (3116)

<400> 1
ttggtgctgg aaagcccatt taagggatct tataaggtaa ttgccaatgt tcagtcgcct 60
atggtcctttg tcgagagaaa ctctttctcg ttaagatcta catgatcgct tttgattttc 120
tctgggttca cgcggtactt tctccccgtc aatccccaac cgctgttgtg cctgaccatc 180
aatgtggaac ggataagggg acaagagaaa ttgaaggagc gatcataaaa agctaatttt 240
ggtttattat ttttttttct tataaaaactc aaaaaagaaa acgaaaacga aaaaggaaaa 300
aagaaaaggt aaaatggaaa aagaaaggcg gtcatcactt ccaataacca tcagccaaag 360
atacagacga gttactgacc ttcttatcct ggacttccgc ccgatccata tcttcatgat 420
aagcagggaa ccgaacaaat caacgccaac ttcagcggca gttcctcact aatttccac 480
ttcccaccgg cgtcattttg gtcccaaccc cctccctgga agcagcggga tttagttacg 540

atccggttta catcggagac tcggaaaata ccatagcgca tgccaatcaa aaccctccc	600
agggtgactg gccagtatca cgaccattg tttctatctt tctagaagac ctgcaggag	660
atggattggc tggccgccgt gctgccgtcc attagcgtct accccaggtc aagaacggac	720
tggacggacc cataaccaat ctaaccaaag ccaatttcgt caattcccag ctggcgagca	780
caatcccatt cccaggggtg gccgccaact gttaaaaggc actatgtgtc tctccacctg	840
cccgcccccc tcgatggcct gcgcgtaata actattctac tgctttttgc ctcttacttg	900
cctcattatt agtattttac tctactctcc agattgcctg ccagcaattg gtccaaagtg	960
gactttgttt gatgac atg act cga acc gtg gac gag atc aaa tac gaa acg	1012
Met Thr Arg Thr Val Asp Glu Ile Lys Tyr Glu Thr	
1 5 10	
cct tct tca tgg gag cac aag agc ttg gac gtt gcc gag gat ggc agg	1060
Pro Ser Ser Trp Glu His Lys Ser Leu Asp Val Ala Glu Asp Gly Arg	
15 20 25	
cga cta gct ccc cat tcc gac act gct cgt ccg aaa ggc cgc ata cga	1108
Arg Leu Ala Pro His Ser Asp Thr Ala Arg Pro Lys Gly Arg Ile Arg	
30 35 40	
cga tcg atg act gcc tgt cac aca tgt cgg aag ctt aaa act aga tgt	1156
Arg Ser Met Thr Ala Cys His Thr Cys Arg Lys Leu Lys Thr Arg Cys	
45 50 55 60	
gat cta gat ccg cgc ggt cat gcg tgc cgt cgc tgt cta tct cta agg	1204
Asp Leu Asp Pro Arg Gly His Ala Cys Arg Arg Cys Leu Ser Leu Arg	
65 70 75	
tcagaggcac tacctacctg ccagttgaag ctttgtcctt ctgaacgcga catgatacta	1264
gtcgtggaat ataactgtcc caactttgct gacagtccac aatatcttta ga atc gat	1322
Ile Asp	
tgt aag ctg cct gaa acg acc gac cgc ttc caa gac agt gct gcg atg	1370
Cys Lys Leu Pro Glu Thr Thr Asp Arg Phe Gln Asp Ser Ala Ala Met	
80 85 90	
tgg cca gac gcc acc tcg gca att ccc tcc atc gag gag cgc ctc acc	1418
Trp Pro Asp Ala Thr Ser Ala Ile Pro Ser Ile Glu Glu Arg Leu Thr	
95 100 105 110	
tcc cta gaa aga tgc atg agg gag atg acg ggc atg atg cga cag atg	1466
Ser Leu Glu Arg Cys Met Arg Glu Met Thr Gly Met Met Arg Gln Met	
115 120 125	
cta gat cac tcc cca ggt ttc gca aat gcc tcg gtt ccg cat ttg acc	1514
Leu Asp His Ser Pro Gly Phe Ala Asn Ala Ser Val Pro His Leu Thr	
130 135 140	
aaa agc atc atc acg gat gaa acc gcc tcg atg gag gga agc ccg tcg	1562

Lys Ser Ile Ile Thr Asp Glu Thr Ala Ser Met Glu Gly Ser Pro Ser	
145 150 155	
tcc ccc ttc ctg cct aag ccc gtt cgc ctc att cag gac ctc cag tcc	1610
Ser Pro Phe Leu Pro Lys Pro Val Arg Leu Ile Gln Asp Leu Gln Ser	
160 165 170	
gac ttc ttc gga gaa gca gag act tcc ccc gtt gac tcc cct ctc tcc	1658
Asp Phe Phe Gly Glu Ala Glu Thr Ser Pro Val Asp Ser Pro Leu Ser	
175 180 185 190	
agc gat ggt aac gcc aag ggc gct atc gac tct aag cta tcc ctc aaa	1706
Ser Asp Gly Asn Ala Lys Gly Ala Ile Asp Ser Lys Leu Ser Leu Lys	
195 200 205	
ttg ttg caa acg tatgggtata cctgattgac aattacaaa aagctgctaa	1758
Leu Leu Gln Thr	
210	
tccttggcgc aaatcagg ttt gtc gat cac ttt ggc gct tgc gtt tcc att	1809
Phe Val Asp His Phe Gly Ala Cys Val Ser Ile	
215 220	
tac aat ctc tcc gac atc cac aac gac atg aaa gcc ccc gac tct tta	1857
Tyr Asn Leu Ser Asp Ile His Asn Asp Met Lys Ala Pro Asp Ser Leu	
225 230 235	
ctg tat aat act gca tgc ctt cta gct tca cgc tat gta ccg ggg ata	1905
Leu Tyr Asn Thr Ala Cys Leu Leu Ala Ser Arg Tyr Val Pro Gly Ile	
240 245 250	
ccg aca tct acc gtg cat gct ata tac ctt caa gtg cga cat gca gta	1953
Pro Thr Ser Thr Val His Ala Ile Tyr Leu Gln Val Arg His Ala Val	
255 260 265	
gtc aat att ttg tgg gaa aaa cca ccc ctg aag tat gag acc ctc caa	2001
Val Asn Ile Leu Trp Glu Lys Pro Pro Leu Lys Tyr Glu Thr Leu Gln	
270 275 280 285	
gca ctt gca ctt ctc tgt ctc tgg cca gca acc gcc cag aaa gag cca	2049
Ala Leu Ala Leu Leu Cys Leu Trp Pro Ala Thr Ala Gln Lys Glu Pro	
290 295 300	
ccc atg gac agc tgg ctg ctg agt ggt atc tca att aac cat gca att	2097
Pro Met Asp Ser Trp Leu Leu Ser Gly Ile Ser Ile Asn His Ala Ile	
305 310 315	
atc gcg ctc gat ttc cta aac tat gcg ccc tcg gaa gtc atg gtg gac	2145
Ile Ala Leu Asp Phe Leu Asn Tyr Ala Pro Ser Glu Val Met Val Asp	
320 325 330	
aat gaa acg gct gcg cag ctg cgg cta tgg aat aca tat tgc ttg aca	2193
Asn Glu Thr Ala Ala Gln Leu Arg Leu Trp Asn Thr Tyr Cys Leu Thr	
335 340 345	
cag cta cag tgggtttcat ctaagatctc ccgtccagaa gatagctaac	2242
Gln Leu Gln	

350

aagctttagt ttt gcg gtc ggg aat gcg cgt cct ttc cat atc cag caa	2291
Phe Ala Val Gly Asn Ala Arg Pro Phe His Ile Gln Gln	
355 360 365	
aga tac ctt gac cac tgc cca cgg ata ctg gag cac cca gca gca act	2339
Arg Tyr Leu Asp His Cys Pro Arg Ile Leu Glu His Pro Ala Ala Thr	
370 375 380	
ctg gag gac gca agg gtt gta gca gaa ata cag ttg tat ttg atg aca	2387
Leu Glu Asp Ala Arg Val Val Ala Glu Ile Gln Leu Tyr Leu Met Thr	
385 390 395	
ttg cgg ctg cag agc aat agc agt cga atg cgg ttg gcg gac ctt gac	2435
Leu Arg Leu Gln Ser Asn Ser Ser Arg Met Arg Leu Ala Asp Leu Asp	
400 405 410	
tat gag gaa ata gag cga tgg aag agg gag tgg gct cac ctt ttc tgt	2483
Tyr Glu Glu Ile Glu Arg Trp Lys Arg Glu Trp Ala His Leu Phe Cys	
415 420 425	
aag aag cct gtt ctt gtt tcc cgg gga cta cca ctg acg aga gca aca	2531
Lys Lys Pro Val Leu Val Ser Arg Gly Leu Pro Leu Thr Arg Ala Thr	
430 435 440 445	
gct ggg gaa agt tcc aca ttg gag ctg agc ctt tgg ttc tgc cag aca	2579
Ala Gly Glu Ser Ser Thr Leu Glu Leu Ser Leu Trp Phe Cys Gln Thr	
450 455 460	
ctc ctt cac cgc aca gca atg agg ctt cag ccc aga tcc gac agg ctc	2627
Leu Leu His Arg Thr Ala Met Arg Leu Gln Pro Arg Ser Asp Arg Leu	
465 470 475	
gca tct gag gtt ctg caa acc tca cgt ctg ata ata tcg cgg ttc ctc	2675
Ala Ser Glu Val Leu Gln Thr Ser Arg Leu Ile Ile Ser Arg Phe Leu	
480 485 490	
cag atc cgg tac tct acc gca tta agc ctt gtc gac caa gtc tat ttc	2723
Gln Ile Arg Tyr Ser Thr Ala Leu Ser Leu Val Asp Gln Val Tyr Phe	
495 500 505	
att gtc ggc tac gct gca ctg aat ctg tgc gat ttc aat ctt atg gac	2771
Ile Val Gly Tyr Ala Ala Leu Asn Leu Cys Asp Phe Asn Leu Met Asp	
510 515 520 525	
ccg ctt atc gag caa gtg cag atg ttc ctg ctg cat ctc tcc ccg aac	2819
Pro Leu Ile Glu Gln Val Gln Met Phe Leu Leu His Leu Ser Pro Asn	
530 535 540	
gaa gac cac atc gcc tac cgg ttt tcg tgc atg gtc gcc gag ttc aag	2867
Glu Asp His Ile Ala Tyr Arg Phe Ser Cys Met Val Ala Glu Phe Lys	
545 550 555	
cgg cga tgt ggc agt gcg gaa tgc aat gac cca tca tcc act gtc aag	2915
Arg Arg Cys Gly Ser Ala Glu Cys Asn Asp Pro Ser Ser Thr Val Lys	
560 565 570	

ggg tct ccg tta tca tcc tac ggc gac agt cgt aag atg agc atg ggg Gly Ser Pro Leu Ser Ser Tyr Gly Asp Ser Arg Lys Met Ser Met Gly 575 580 585	2963
caa gca ccg ttc atg cca ccg ctc atg gat ggc atg atc gag ggg tac Gln Ala Pro Phe Met Pro Pro Leu Met Asp Gly Met Ile Glu Gly Tyr 590 595 600 605	3011
ggc ttc gag caa ctg atg cca gaa gtc atg ccg agt tcc ttt ccg gat Gly Phe Glu Gln Leu Met Pro Glu Val Met Pro Ser Ser Phe Pro Asp 610 615 620	3059
ggg ata ctc aac gga atg cct gtg act ggg cta gca gcg tat cgg tca Gly Ile Leu Asn Gly Met Pro Val Thr Gly Leu Ala Ala Tyr Arg Ser 625 630 635	3107
gcg acg ctg taagtaatcg agatcggggtt ggaaaggaca tgagtggggg Ala Thr Leu 640	3156
tggtggtggt agtagcagta acaccaggga tgataacctg cagcgggtggt ttagttcctg	3216
cccatgggct gaactaaaac cccgaaccta gcatgatgac gtgcaacgaa aggatcataa	3276
ccaaggccaa gtaaatacta aaataaaata atataattcc acacgatcca ctaccaccac	3336
caccaccgga tccatcaggt tgccttcctg cacaggccta tttagttaga gggcccgtgc	3396
cacgaaacat cacgtaattg agcgcttttg cttccttgca acttaaaciaa ccccatagac	3456
actctcacat tcacatgcca aactactaac tcctactgac caccagctgc aggaagccag	3516
ccagccacca tttcctaate ggatataatc ccgaaacgta cgctttcctc ctttgttcgg	3576
accgttcctg gcctccgagg agagttgaac gagtcagaac acattctttt cgtttctatc	3636
gtttcttttc caaggcagca gagagacgaa caagtcagtg cttgctaact aacttacccc	3696
tcagcatttt agtaaactac tatttaggaa agagtaatca ttcacgaag acaagatgtt	3756
tatttctccg atcgaccaa caaaaacgtt caggtagact aagtagtagt agtagtatgt	3816
ctttgacccc tttactccac tatccgttga ctgcacatag tagtaagtaa ctatctaacc	3876
agttgccgag gagaggaaag tgagtgggtg ggagccggag gatgccgccg agaattatta	3936
agtcgatcat tgctagttag ttatcttttc atgatgagga gaggaaggag aggggggacg	3996
ggattagaga aataaacttt tctctccaat taattatctg gattaattaa aacttggaga	4056
ggagggtagg ggagttgggt attggtatgt tgctgtgaat gt	4098
 <210> 2	
<211> 666	
<212> PRT	

<213> Aspergillus niger

<400> 2

Met	Thr	Arg	Thr	Val	Asp	Glu	Ile	Lys	Tyr	Glu	Thr	Pro	Ser	Ser	Trp
1				5					10					15	
Glu	His	Lys	Ser	Leu	Asp	Val	Ala	Glu	Asp	Gly	Arg	Arg	Leu	Ala	Pro
			20					25					30		
His	Ser	Asp	Thr	Ala	Arg	Pro	Lys	Gly	Arg	Ile	Arg	Arg	Ser	Met	Thr
		35					40					45			
Ala	Cys	His	Thr	Cys	Arg	Lys	Leu	Lys	Thr	Arg	Cys	Asp	Leu	Asp	Pro
	50					55					60				
Arg	Gly	His	Ala	Cys	Arg	Arg	Cys	Leu	Ser	Leu	Arg	Ile	Asp	Cys	Lys
65					70					75					80
Leu	Pro	Glu	Thr	Thr	Asp	Arg	Phe	Gln	Asp	Ser	Ala	Ala	Met	Trp	Pro
				85					90					95	
Asp	Ala	Thr	Ser	Ala	Ile	Pro	Ser	Ile	Glu	Glu	Arg	Leu	Thr	Ser	Leu
			100					105					110		
Glu	Arg	Cys	Met	Arg	Glu	Met	Thr	Gly	Met	Met	Arg	Gln	Met	Leu	Asp
		115					120					125			
His	Ser	Pro	Gly	Phe	Ala	Asn	Ala	Ser	Val	Pro	His	Leu	Thr	Lys	Ser
		130				135					140				
Ile	Ile	Thr	Asp	Glu	Thr	Ala	Ser	Met	Glu	Gly	Ser	Pro	Ser	Ser	Pro
145					150					155					160
Phe	Leu	Pro	Lys	Pro	Val	Arg	Leu	Ile	Gln	Asp	Leu	Gln	Ser	Asp	Phe
			165						170					175	
Phe	Gly	Glu	Ala	Glu	Thr	Ser	Pro	Val	Asp	Ser	Pro	Leu	Ser	Ser	Asp
			180					185					190		
Gly	Asn	Ala	Lys	Gly	Ala	Ile	Asp	Ser	Lys	Leu	Ser	Leu	Lys	Leu	Leu
		195					200					205			
Gln	Thr	Phe	Val	Asp	His	Phe	Gly	Ala	Cys	Val	Ser	Ile	Tyr	Asn	Leu
		210				215					220				
Ser	Asp	Ile	His	Asn	Asp	Met	Lys	Ala	Pro	Asp	Ser	Leu	Leu	Tyr	Asn
225				230						235					240
Thr	Ala	Cys	Leu	Leu	Ala	Ser	Arg	Tyr	Val	Pro	Gly	Ile	Pro	Thr	Ser
			245						250					255	
Thr	Val	His	Ala	Ile	Tyr	Leu	Gln	Val	Arg	His	Ala	Val	Val	Asn	Ile
			260				265						270		
Leu	Trp	Glu	Lys	Pro	Pro	Leu	Lys	Tyr	Glu	Thr	Leu	Gln	Ala	Leu	Ala
		275					280					285			

Leu	Leu	Cys	Leu	Trp	Pro	Ala	Thr	Ala	Gln	Lys	Glu	Pro	Pro	Met	Asp	290	295	300	
Ser	Trp	Leu	Leu	Ser	Gly	Ile	Ser	Ile	Asn	His	Ala	Ile	Ile	Ala	Leu	305	310	315	320
Asp	Phe	Leu	Asn	Tyr	Ala	Pro	Ser	Glu	Val	Met	Val	Asp	Asn	Glu	Thr	325	330	335	
Ala	Ala	Gln	Leu	Arg	Leu	Trp	Asn	Thr	Tyr	Cys	Leu	Thr	Gln	Leu	His	340	345	350	
Phe	Ala	Val	Gly	Asn	Ala	Arg	Pro	Phe	His	Ile	Gln	Gln	Arg	Tyr	Leu	355	360	365	
Asp	His	Cys	Pro	Arg	Ile	Leu	Glu	His	Pro	Ala	Ala	Thr	Leu	Glu	Asp	370	375	380	
Ala	Arg	Val	Val	Ala	Glu	Ile	Gln	Leu	Tyr	Leu	Met	Thr	Leu	Arg	Leu	385	390	395	400
Gln	Ser	Asn	Ser	Ser	Arg	Met	Arg	Leu	Ala	Asp	Leu	Asp	Tyr	Glu	Glu	405	410	415	
Ile	Glu	Arg	Trp	Lys	Arg	Glu	Trp	Ala	His	Leu	Phe	Cys	Lys	Lys	Pro	420	425	430	
Val	Leu	Val	Ser	Arg	Gly	Leu	Pro	Leu	Thr	Arg	Ala	Thr	Ala	Gly	Glu	435	440	445	
Ser	Ser	Thr	Leu	Glu	Leu	Ser	Leu	Trp	Phe	Cys	Gln	Thr	Leu	Leu	His	450	455	460	
Arg	Thr	Ala	Met	Arg	Leu	Gln	Pro	Arg	Ser	Asp	Arg	Leu	Ala	Ser	Glu	465	470	475	480
Val	Leu	Gln	Thr	Ser	Arg	Leu	Ile	Ile	Ser	Arg	Phe	Leu	Gln	Ile	Arg	485	490	495	
Tyr	Ser	Thr	Ala	Leu	Ser	Leu	Val	Asp	Gln	Val	Tyr	Phe	Ile	Val	Gly	500	505	510	
Tyr	Ala	Ala	Leu	Asn	Leu	Cys	Asp	Phe	Asn	Leu	Met	Asp	Pro	Leu	Ile	515	520	525	
Glu	Gln	Val	Gln	Met	Phe	Leu	Leu	His	Leu	Ser	Pro	Asn	Glu	Asp	His	530	535	540	
Ile	Ala	Tyr	Arg	Phe	Ser	Cys	Met	Val	Ala	Glu	Phe	Lys	Arg	Arg	Cys	545	550	555	560
Gly	Ser	Ala	Glu	Cys	Asn	Asp	Pro	Ser	Ser	Thr	Val	Lys	Gly	Ser	Pro	565	570	575	
Leu	Ser	Ser	Tyr	Gly	Asp	Ser	Arg	Lys	Met	Ser	Met	Gly	Gln	Ala	Pro	580	585	590	

Phe Met Pro Pro Leu Met Asp Gly Met Ile Glu Gly Tyr Gly Phe Glu
595 600 605

Gln Leu Met Pro Glu Val Met Pro Ser Ser Phe Pro Asp Gly Ile Leu
610 615 620

Asn Gly Met Pro Val Thr Gly Leu Ala Ala Tyr Arg Ser Ala Thr Leu
625 630 635 640

Ser Ser Asn Thr Arg Asp Asp Asn Leu Gln Arg Trp Phe Ser Ser Cys
645 650 655

Pro Trp Ala Glu Leu Lys Pro Arg Thr Pro
660 665

<210> 3
<211> 35
<212> PRT
<213> Aspergillus niger

<400> 3

Met Thr Ala Cys His Thr Cys Arg Lys Leu Lys Thr Arg Cys Asp Leu
1 5 10 15

Asp Pro Arg Gly His Ala Cys Arg Arg Cys Leu Ser Leu Arg Ile Asp
20 25 30

Cys Lys Leu
35

<210> 4
<211> 2542
<212> DNA
<213> Artificial

<220>
<223> Synthetic

<400> 4
gacatggatt ggctggccgc cgtgctgccg tccattagcg tctaccccag gtcaagaacg 60
gactggacgg acccataacc aatctaacca aagccaattt cgtcaattcc cagctggcga 120
gcacaatccc attcccaggg ttggccgcca actgttaaaa ggcactatgt gtctctccac 180
ctgcccgcgc cctcgatgg cctgcgcgta ataactattc tactgctttt tgctctttac 240
ttgcctcatt attagtattt tactctactc tccagattgc ctgccagcaa ttggtccaaa 300
gtggactttg tttgatgaca tgactcgaac cgtggacgag atcaaatacg aaacgccttc 360
ttcatgggag cacaagagct tggacgttgc cgaggatggc aggcgactag ctccccattc 420
cgacactgct cgtccgaaag gccgcatacg acgatcgatg actgcctgtc acacatgtcg 480

gaagcttaaa actagatgtg atctagatcc gcgcgggtcat gcgtgccgtc gctgtctatc	540
tctaagggtca gaggcactac ctacctgcca gttgaagctt tgtccttctg aacgcgacat	600
gatactagtc gtggaatata actgtcccaa ctttgctgac agtccacaat atcttttagaa	660
tcgattgtaa gctgcctgaa acgaccgacc gcttccaaga cagtgcctgcg atgtggccag	720
acgccacctc ggcaattccc tccatcgagg agcgccctcac ctccctagaa agatgcatga	780
gggagatgac gggcatgatg cgacagatgc tagatcactc cccaggtttc gcaaatgcct	840
cggttccgca tttgaccaa agcatcatca cggatgaaac cgcctcgatg gagggagacc	900
cgtcgtcccc cttcctgcct aagcccgttc gcctcattca ggacctccag tccgacttct	960
tcggagaagc agagacttcc cccgttgact cccctctctc cagcgatggg aacgccaagg	1020
gcgctatcga ctctaagcta tccctcaa atgttgcaaac gtatgggtat acctgattga	1080
caattacca aaagctgcta atccttggcg caaatcaggt ttgtcgatca ctttggcgct	1140
tgcgtttcca tttacaatct ctccgacatc cacaacgaca tgaaagcccc cgactcttta	1200
ctgtataata ctgcatgcct tctagcttca cgctatgtac cggggatacc gacatctacc	1260
gtgcatgcta tataccttca agtgcgacat gcagtagtca atattttgtg ggaaaaacca	1320
cccctgaagt atgagaccct ccaagcactt gcacttctct gtctctggcc agcaaccgcc	1380
cagaaagagc caccatgga cagctggctg ctgagtggta tctcaattaa ccatgcaatt	1440
atcgcgctcg atttcctaaa ctatgcgccc tcggaagtca tgggtggaaa tgaaacggct	1500
gcgcagctgc ggctatggaa tacatattgc ttgacacagc tacagtgggt ttcatctaag	1560
atctcccgtc cagaagatag ctaacaagct ttagttttgc ggtcggaat gcgcgtcctt	1620
tccatatcca gcaagatac cttgaccact gccacggat actggagcac ccagcagcaa	1680
ctctggagga cgcaagggtt gtagcagaaa tacagttgta tttgatgaca ttgcggctcc	1740
agagcaatag cagtcgaatg cggttggcgg accttgacta tgaggaaata gagcgatgga	1800
agagggagtg ggctcacctt ttctgtaaga agcctgttct tgtttcccg ggactaccac	1860
tgacgagagc aacagctggg gaaagttcca cattggagct gagcctttgg ttctgccaga	1920
cactccttca ccgcacagca atgaggcttc agcccagatc cgacaggctc gcatctgagg	1980
ttctgcaaac ctcacgtctg ataatatcgc ggttcctcca gatccggtac tctaccgcat	2040
taagccttgt cgaccaagtc tatttcattg tcggctacgc tgactgaat ctgtgcgatt	2100
tcaatcttat ggaccgctt atcgagcaag tgcagatggt cctgctgcat ctctccccga	2160
acgaagacca catcgcttac cggttttcgt gcatggctgc cgagttcaag cggcgatgtg	2220

gcagtgcgga atgcaatgac ccatcatcca ctgtcaaggg gtctccgtta tcatcctacg 2280
gcgacagtcg taagatgagc atggggcaag caccgttcat gccaccgctc atggatggca 2340
tgatcgaggg gtacggcttc gagcaactga tgccagaagt catgccgagt tcctttccgg 2400
atgggatact caacggaatg cctgtgactg ggctagcagc gtatcgggtca gcgacgctgt 2460
aagtaatcga gatcgggttg gaaaggacat gagtgggggt ggtgggtgga gtagcagtaa 2520
caccagggat gataacctgc ag 2542

<210> 5
<211> 665
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 5

Met	Thr	Arg	Thr	Val	Asp	Glu	Ile	Lys	Tyr	Glu	Thr	Pro	Ser	Ser	Trp
1				5					10					15	
Glu	His	Lys	Ser	Leu	Asp	Val	Ala	Glu	Asp	Gly	Arg	Arg	Leu	Ala	Pro
			20					25					30		
His	Ser	Asp	Thr	Ala	Arg	Pro	Lys	Gly	Arg	Ile	Arg	Arg	Ser	Met	Thr
			35				40					45			
Ala	Cys	His	Thr	Cys	Arg	Lys	Leu	Lys	Thr	Arg	Cys	Asp	Leu	Asp	Pro
	50					55					60				
Arg	Gly	His	Ala	Cys	Arg	Arg	Cys	Leu	Ser	Leu	Arg	Ile	Asp	Cys	Lys
65					70					75				80	
Leu	Pro	Glu	Thr	Thr	Asp	Arg	Phe	Gln	Asp	Ser	Ala	Ala	Met	Trp	Pro
				85					90					95	
Asp	Ala	Thr	Ser	Ala	Ile	Pro	Ser	Ile	Glu	Glu	Arg	Leu	Thr	Ser	Pro
			100					105					110		
Glu	Arg	Cys	Met	Arg	Glu	Met	Thr	Gly	Met	Met	Arg	Gln	Met	Leu	Asp
		115					120					125			
His	Ser	Pro	Gly	Phe	Ala	Asn	Ala	Ser	Val	Pro	His	Leu	Thr	Lys	Ser
	130					135					140				
Ile	Ile	Thr	Asp	Glu	Thr	Ala	Ser	Met	Glu	Gly	Ser	Pro	Ser	Ser	Pro
145					150					155					160
Phe	Leu	Pro	Lys	Pro	Val	Arg	Leu	Ile	Gln	Asp	Leu	Gln	Ser	Asp	Phe
				165					170					175	

Phe Gly Glu Ala Glu Thr Ser Pro Val Asp Ser Pro Leu Ser Ser Asp
180 185 190
Gly Asn Ala Lys Gly Ala Ile Asp Ser Lys Leu Ser Leu Lys Leu Leu
195 200 205
Gln Thr Phe Val Asp His Phe Gly Ala Cys Val Ser Ile Tyr Asn Leu
210 215 220
Ser Asp Ile His Asn Asp Met Lys Ala Pro Asp Ser Leu Leu Tyr Asn
225 230 235 240
Thr Ala Cys Leu Leu Ala Ser Arg Tyr Val Pro Gly Ile Pro Thr Ser
245 250 255
Thr Val His Ala Ile Tyr Leu Gln Val Arg His Ala Val Val Asn Ile
260 265 270
Leu Trp Glu Lys Pro Pro Leu Lys Tyr Glu Thr Leu Gln Ala Leu Ala
275 280 285
Leu Leu Cys Leu Trp Pro Ala Thr Ala Gln Lys Glu Pro Pro Met Asp
290 295 300
Ser Trp Leu Leu Ser Gly Ile Ser Ile Asn His Ala Ile Ile Ala Leu
305 310 315 320
Asp Phe Leu Asn Tyr Ala Pro Ser Glu Val Met Val Asp Asn Glu Thr
325 330 335
Ala Ala Gln Leu Arg Leu Trp Asn Thr Tyr Cys Leu Thr Gln Leu His
340 345 350
Phe Ala Val Gly Asn Ala Arg Pro Phe His Ile Gln Gln Arg Tyr Leu
355 360 365
Asp His Cys Pro Arg Ile Leu Glu His Pro Ala Ala Thr Leu Glu Asp
370 375 380
Ala Arg Val Val Ala Glu Ile Gln Leu Tyr Leu Met Thr Leu Arg Leu
385 390 395 400
Gln Ser Asn Ser Ser Arg Met Arg Leu Ala Asp Leu Asp Tyr Glu Glu
405 410 415
Ile Glu Arg Trp Lys Arg Glu Trp Ala His Leu Phe Cys Lys Lys Pro
420 425 430
Val Leu Val Ser Arg Gly Leu Pro Leu Thr Arg Ala Thr Ala Gly Glu
435 440 445
Ser Ser Thr Leu Glu Leu Ser Leu Trp Phe Cys Gln Thr Leu Leu His
450 455 460
Arg Thr Ala Met Arg Leu Gln Pro Arg Ser Asp Arg Leu Ala Ser Glu
465 470 475 480

Val Leu Gln Thr Ser Arg Leu Ile Ile Ser Arg Phe Leu Gln Ile Arg
 485 490 495
 Tyr Ser Thr Ala Leu Ser Leu Val Asp Gln Val Tyr Phe Ile Val Gly
 500 505 510
 Tyr Ala Ala Leu Asn Leu Cys Asp Phe Asn Leu Met Asp Pro Leu Ile
 515 520 525
 Glu Gln Val Gln Met Phe Leu Leu His Leu Ser Pro Asn Glu Asp His
 530 535 540
 Ile Ala Tyr Arg Phe Ser Cys Met Val Ala Glu Phe Lys Arg Arg Cys
 545 550 555 560
 Gly Ser Ala Glu Cys Asn Asp Pro Ser Ser Thr Val Lys Gly Ser Pro
 565 570 575
 Leu Ser Ser Tyr Gly Asp Ser Arg Lys Met Ser Met Gly Gln Ala Pro
 580 585 590
 Phe Met Pro Pro Leu Met Asp Gly Met Ile Glu Gly Tyr Gly Phe Glu
 595 600 605
 Gln Leu Met Pro Glu Val Met Pro Ser Ser Phe Pro Asp Gly Ile Leu
 610 615 620
 Asn Gly Met Pro Val Thr Gly Leu Ala Ala Tyr Arg Ser Ala Thr Leu
 625 630 635 640
 Ser Ser Asn Thr Arg Asp Asp Asn Leu Gln Arg Trp Phe Ser Ser Cys
 645 650 655
 Pro Trp Ala Glu Leu Lys Pro Arg Thr
 660 665

<210> 6
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<400> 6
 cggaattcgc atgctggagg tgcttctaa

29

<210> 7
 <211> 33
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<400> 7

ttcccaggat tgaggcattt tgaccacgag att 33

<210> 8
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 8
taacttccac cgaggtc 17

<210> 9
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 9
cgatcgatga ctgcctgt 18

<210> 10
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 10
agagacacat agtgcctt 18

<210> 11
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 11
gcttatagtc gatagcgc 18

<210> 12
<211> 18
<212> DNA
<213> Artificial

<220>

<223> Primer

<400> 12
cctctctcca gcgatggt 18

<210> 13
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 13
atggaataca tactgctt 18

<210> 14
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 14
atgaaaccca ctgtagct 18

<210> 15
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 15
tgctcgataa gcgggtcc 18

<210> 16
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 16
attcttatgg acccgctt 18

<210> 17
<211> 20
<212> DNA

<213> Artificial
 <220>
 <223> Primer
 <400> 17
 ccccgaggaaa caagaacagg 20
 <210> 18
 <211> 20
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer
 <400> 18
 gttggcggac cttgactatg 20
 <210> 19
 <211> 22
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer
 <400> 19
 acagctacag tgggtttcat ct 22
 <210> 20
 <211> 19
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer
 <400> 20
 agtcaacggg ggaagtctc 19
 <210> 21
 <211> 20
 <212> DNA
 <213> Artificial
 <220>
 <223> Primer
 <400> 21
 ctagcagcgt atcggtcagc 20

<210>	22	
<211>	19	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	22	
	cttggaaaag aaacgatag	19
<210>	23	
<211>	19	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	23	
	aacgtacgct ttcctcctt	19
<210>	24	
<211>	21	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	24	
	gggtccgtcc agtccgttct t	21
<210>	25	
<211>	24	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	25	
	agcggataac aatttcacac agga	24
<210>	26	
<211>	17	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	26	

gttttcccag tcacgac 17

<210> 27
<211> 19
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 27
tcatccctgg tggtactgc 19

<210> 28
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 28
catggattgg ctggccg 17

<210> 29
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 29
tactctccag attgcctg 18

<210> 30
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 30
tgagatacca ctcagcag 18

<210> 31
<211> 18
<212> DNA
<213> Artificial

<220>

<223> Primer

<400> 31

tgcacttctc tgtctctg

18

<210> 32

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 32

gacttctggc atcagttg

18

<210> 33

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 33

ctcatggatg gcatgatc

18

<210> 34

<211> 33

<212> PRT

<213> Aspergillus niger

<400> 34

Met Thr Ala Cys His Thr Cys Arg Lys Leu Lys Thr Arg Cys Asp Leu
1 5 10 15

Asp Pro Arg Gly His Ala Cys Arg Arg Cys Leu Ser Leu Arg Ile Asp
20 25 30

Cys

<210> 35

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 35

atgacygcyt gycayacytg

20

<210>	36	
<211>	20	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<220>		
<221>	n	
<222>	(9)..(9)	
<223>	any dna molecule	
<400>	36	
	arrcancgnc grcargcrtg	20
<210>	37	
<211>	20	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	37	
	atgactgcct gtcacacatg	20
<210>	38	
<211>	20	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	38	
	agacagcgac ggcacgcatg	20
<210>	39	
<211>	21	
<212>	DNA	
<213>	Artificial	
<220>		
<223>	Primer	
<400>	39	
	caccgagttt taagcttgcg g	21
<210>	40	
<211>	20	

<212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 40
 gcgatcttga tccacgaggg 20

 <210> 41
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 41
 cgggatgaat thtagagagg c 21

 <210> 42
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 42
 cgcaagctta aaactcgggtg cgatc 25

 <210> 43
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 43
 cctcgtggat caagatcgca 20

 <210> 44
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 44
 gatgaaaaga ataatcggcg ag 22

<210> 45
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 45
 cgcggcacac tacccccgtt g 21

 <210> 46
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 46
 atctagctca agcattagcg gc 22

 <210> 47
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Primer

 <400> 47
 aatttcggcc ctttagtgtc c 21

 <210> 48
 <211> 2931
 <212> DNA
 <213> *Aspergillus oryzae*

 <220>
 <221> Intron
 <222> (1028)..(1135)

 <220>
 <221> Intron
 <222> (1538)..(1591)

 <220>
 <221> Intron
 <222> (2018)..(2066)

 <220>
 <221> Intron
 <222> (2297)..(2347)

<400> 48

gatatctcat gatctgctg atcggttgc ctcctatctt agatcacccg ggcttcttca	60
aatcagcaac aacgctcaga catgtcccct gagaggatgat ccaaatacata cacgagagaa	120
cgcggaacg caaattaagg atgagcgaaa aagagaaaaa aatccgttgt tcctgagtca	180
tgacgaatga gcaaaagtca aacacacctt ctgcttttgg ggggtatgcc cgatcacaat	240
cttcaaccgg ccatgataag agacacacgc tatcgacaaa tcaccggagg tcaagattag	300
tggcagtcct tagctaattt cagggtcggcg tcaaccttag ccaaccaaac ccaaccccct	360
catggaagcg ggactcccta tggagccggc ttacatcggg cgactgcaa tggcgcacgt	420
caatcaaccc ctctcttgtt gcagtgccta gtatgccaaa ccaccctttc tattcttcta	480
gaaaccacac cctagagact cggatctaca cggattgggt ggaatgctcc gattagttgg	540
catttaccac aggtcaaaat ggataatcaa tctaacggag tctatttcgt caactgcctg	600
ccagctagca caatctcctc ttcacgcccg gccgtgggct gttaaaaggg tcaattccct	660
ccccacctgt gtggattctc tatgatttgc acgggatctg acttggtttc cacaattctt	720
cttgctctca gcttgttcta ctgcgcgatt attcttttca tcaacgcggc aactacccc	780
cggtgtctga tgtcatgact agaactactg ttgaacctat caaatatgag gcccttcgt	840
gggagcataa gagcgtgcat gtgtccgacg accacaggag aatcatcccc aatgtcggcg	900
acgacgcgac gcgcccagg ggccgcatta gacgttcaat gaccgcttgt aatacctgcc	960
gcaagcttaa aactcgggtgc gatcttgatc cacgagggca tgcattgccg cgggtgtctat	1020
ctttaagggtc ggggtgccacc gttatccact ttgtcaaata tcttacgtca aaatggggga	1080
tcccatgtcc tgccaagacc aaataagcct ttcttgagta ctaatgtttc tataggatcg	1140
actgtcagct ccccgagacg agtgagcgtc ttcaggacag tactccaatg tggtcagacg	1200
caacgacagc tatccccctc atcgaggagc gtctcacttc cctagagagg agtatgagag	1260
agatgaccgg catgcttcgg cagatcttga atcaatcacc aagcgtctct aatatctccg	1320
tcctccgct agctcggagt gttcatcagg aagaaacggc ctccattgaa ggaaactcat	1380
tcggtccttt cctacctaaa cccgttcggc taattcagga cctccaatct gagttttttg	1440
gggagacaaa ccgcatccct gttgaatctc ctttcttggg taacagtttt gagaagggtta	1500
tcttagattc taagttgtct ctcaagttgg tacagctgta tggtcactcg tcatgtccat	1560
ctgcctctat agccgctaata gcttgagcta gatttggtga taatttcggc ctttagtgt	1620
ccataaataa tcagtcggac ttccacaacg agatgaggaa caccgattcg ttgttatata	1680

gtactgcctg tcttctggcc tcccgatatg tgccaggcat accaccaccg attgtccata 1740
 ccatgaacct ccaagttcga cataaggcag tcaatctgct gtgggaagaa cgccttttga 1800
 aatacgaatc gctccaggca ctgcccttc tttgtttatg gccagcggcg ggtcaaaagg 1860
 agttcccat agatggctgg ttactgagcg ggactgcaat caatcatgcc ctctctcct 1920
 ttgacttcct caatcatgtg ccttcagagc ttctcattga taacgatatc gccgctcaat 1980
 tgcggctctg gaacgctttc tgtttaacac agttacagta ggtacaacat ttccggctta 2040
 actccaactt gctaattgcag aaatagtttc gctgttggca acgcacgtcc attccattta 2100
 ccacagagat atctcgatta ttgcccacga cttcttgagc accccgctgc aacagttgag 2160
 gatggcaagg tcgtagcaga gatccagttg tacttgatca cattgcgact ccaagccaac 2220
 gagcaacgta tgcgattcgc ggaggttgaa tacgaagaga ttgaacgatg gaaagttgaa 2280
 tgggcccac tcttggttaa ggtaagcaa cgaggaccat ctcatataaa tgctaactat 2340
 tcaacagctg gtgatgaaaa ttcaacattt gagcttagtc tctggttctg tcaaattctc 2400
 ctgcatcggc cagcaatgag gttccaagcg gagtctgaga gactcacgtc ggaaattctc 2460
 caaggatcgc gcttgatcat ctcgaaattc ctgcaactcc gatttgtcac cgctctaaga 2520
 gtggtcgatc aggcgtactt catcgtcggt tatgccgctc taaatctttg cgacttcaac 2580
 ttcctcgacc ccctcattga ccagatccag atgtttctgc tgcattctgc gccaaacgaa 2640
 gaccacatcg cataccggtt ttcgtgcatg atagccgagt tcaagcgtcg ctgtgccgaa 2700
 tgcaacgacc cttgcagcgc agtcgacggt tctcaatgct cgttcggaga tgcccggag 2760
 atgagcatgg aacaggtaca attcgtgcca ccactagtag atagcatgat tgggggatat 2820
 agcgtcttgg aacagctgat ccctgaggtc atgccacact catttccgga aagtgtcata 2880
 agtggcatgg ctgtgactga agccatccct gtgggatcgg cgccatacta g 2931

<210> 49
 <211> 624
 <212> PRT
 <213> *Aspergillus oryzae*

<400> 49

Met	Thr	Arg	Thr	Thr	Val	Glu	Pro	Ile	Lys	Tyr	Glu	Ala	Pro	Ser	Trp
1			5					10					15		
Glu	His	Lys	Ser	Val	His	Val	Ser	Asp	Asp	His	Gly	Arg	Ile	Ile	Pro
	20						25					30			

Asn	Val	Gly	Asp	Asp	Ala	Thr	Arg	Pro	Lys	Gly	Arg	Ile	Arg	Arg	Ser	35	40	45	
Met	Thr	Ala	Cys	Asn	Thr	Cys	Arg	Lys	Leu	Lys	Thr	Arg	Cys	Asp	Leu	50	55	60	
Asp	Pro	Arg	Gly	His	Ala	Cys	Arg	Arg	Cys	Leu	Ser	Leu	Arg	Ile	Asp	65	70	75	80
Cys	Gln	Leu	Pro	Glu	Thr	Ser	Glu	Arg	Phe	Gln	Asp	Ser	Thr	Pro	Met	85	90	95	
Trp	Ser	Asp	Ala	Thr	Thr	Ala	Ile	Pro	Ser	Ile	Glu	Glu	Arg	Leu	Thr	100	105	110	
Ser	Leu	Glu	Arg	Ser	Met	Arg	Glu	Met	Thr	Gly	Met	Leu	Arg	Gln	Ile	115	120	125	
Leu	Asn	Gln	Ser	Pro	Ser	Val	Ser	Asn	Ile	Ser	Val	Pro	Pro	Leu	Ala	130	135	140	
Arg	Ser	Val	His	Thr	Glu	Glu	Thr	Ala	Ser	Ile	Glu	Gly	Asn	Ser	Phe	145	150	155	160
Gly	Pro	Phe	Leu	Pro	Lys	Pro	Val	Arg	Leu	Ile	Gln	Asp	Leu	Gln	Ser	165	170	175	
Glu	Phe	Phe	Gly	Glu	Thr	Asn	Arg	Ile	Pro	Val	Glu	Ser	Pro	Phe	Leu	180	185	190	
Gly	Asn	Ser	Phe	Glu	Lys	Gly	Ile	Leu	Asp	Ser	Lys	Leu	Ser	Leu	Lys	195	200	205	
Leu	Val	Gln	Leu	Phe	Val	Asp	Asn	Phe	Gly	Pro	Leu	Val	Ser	Ile	Asn	210	215	220	
Asn	Gln	Ser	Asp	Phe	His	Asn	Glu	Met	Arg	Asn	Thr	Asp	Ser	Leu	Leu	225	230	235	240
Tyr	Ser	Thr	Ala	Cys	Leu	Leu	Ala	Ser	Arg	Tyr	Val	Pro	Gly	Ile	Pro	245	250	255	
Pro	Pro	Ile	Val	His	Thr	Met	Asn	Leu	Gln	Val	Arg	His	Lys	Ala	Val	260	265	270	
Asn	Leu	Leu	Trp	Glu	Glu	Pro	Pro	Leu	Lys	Tyr	Glu	Ser	Leu	Gln	Ala	275	280	285	
Leu	Ala	Leu	Leu	Cys	Leu	Trp	Pro	Ala	Ala	Gly	Gln	Lys	Glu	Phe	Pro	290	295	300	
Ile	Asp	Gly	Trp	Leu	Leu	Ser	Gly	Thr	Ala	Ile	Asn	His	Ala	Leu	Val	305	310	315	320
Ser	Phe	Asp	Phe	Leu	Asn	His	Val	Pro	Ser	Glu	Leu	Leu	Ile	Asp	Asn	325	330	335	

Asp Ile Ala Ala Gln Leu Arg Leu Trp Asn Ala Phe Cys Leu Thr Gln
 340 345 350
 Leu His Phe Ala Val Gly Asn Ala Arg Pro Phe His Leu Pro Gln Arg
 355 360 365
 Tyr Leu Asp Tyr Cys Pro Arg Leu Leu Glu His Pro Ala Ala Thr Val
 370 375 380
 Glu Asp Gly Lys Val Val Ala Glu Ile Gln Leu Tyr Leu Ile Thr Leu
 385 390 395 400
 Arg Leu Gln Ala Asn Glu Gln Arg Met Arg Phe Ala Glu Val Glu Tyr
 405 410 415
 Glu Glu Ile Glu Arg Trp Lys Val Glu Trp Ala His Leu Leu Ala Gly
 420 425 430
 Asp Glu Asn Ser Thr Phe Glu Leu Ser Leu Trp Phe Cys Gln Ile Leu
 435 440 445
 Leu His Arg Thr Ala Met Arg Phe Gln Ala Glu Ser Glu Arg Leu Thr
 450 455 460
 Ser Glu Ile Leu Gln Gly Ser Arg Leu Ile Ile Ser Lys Phe Leu Gln
 465 470 475 480
 Leu Arg Phe Val Thr Ala Leu Arg Val Val Asp Gln Ala Tyr Phe Ile
 485 490 495
 Val Gly Tyr Ala Ala Leu Asn Leu Cys Asp Phe Asn Phe Leu Asp Pro
 500 505 510
 Leu Ile Asp Gln Ile Gln Met Phe Leu Leu His Leu Ser Pro Asn Glu
 515 520 525
 Asp His Ile Ala Tyr Arg Phe Ser Cys Met Ile Ala Glu Phe Lys Arg
 530 535 540
 Arg Cys Ala Glu Cys Asn Asp Pro Cys Ser Ala Val Asp Gly Ser Gln
 545 550 555 560
 Cys Ser Phe Gly Asp Ala Arg Lys Met Ser Met Glu Gln Val Gln Phe
 565 570 575
 Val Pro Pro Leu Val Asp Ser Met Ile Gly Gly Tyr Ser Ala Leu Glu
 580 585 590
 Gln Leu Ile Pro Glu Val Met Pro His Ser Phe Pro Glu Ser Val Ile
 595 600 605
 Ser Gly Met Ala Val Thr Glu Ala Ile Pro Val Gly Ser Ala Pro Tyr
 610 615 620

<210> 50
 <211> 6015
 <212> DNA

<213> Artificial

<220>

<223> pDV8 plasmid

<400> 50

gaatacacgg aattcctcga gtaccattta attctatttg tgtttgatcg agacctaata	60
cagcccctac aacgaccatc aaagtcgtat agctaccagt gaggaagtgg actcaaatcg	120
acttcagcaa catctcctgg ataaacttta agcctaaact atacagaata agataggtgg	180
agagcttata ccgagctccc aaatctgtcc agatcatggg tgaccggtgc ctggatcttc	240
ctatagaatc atccttattc gttgacctag ctgattctgg agtgaccag aggggtcatga	300
cttgagccta aaatccgccg cctccaccat ttgtagaaaa atgtgacgaa ctctgtgagct	360
ctgtacagtg accggtgact ctttctggca tgcggagaga cggacggacg cagagagaag	420
ggctgagtaa taagccactg gccagacagc tctggcggct ctgaggtgca gtggatgatt	480
attaatccgg gaccggccgc ccctccgcc cgaagtggaa aggctggtgt gcccctcggt	540
gaccaagaat ctattgcatc atcggagaat atggagcttc atcgaatcac cggcagtaag	600
cgaaggagaa tgtgaagcca ggggtgtata gccgtcggcg aaatagcatg ccattaacct	660
aggtagagaa gtccaattgc ttccgatctg gtaaaagatt cacgagatag taccttctcc	720
gaagtaggta gagcgagtac ccggcgcgta agctccctaa ttggcccatc cggcatctgt	780
agggcgcca aatatcgtgc ctctcctgct ttgcccgggtg tatgaaaccg gaaaggccgc	840
tcaggagctg gccagcggcg cagaccggga acacaagctg gcagtcgacc catccgggtgc	900
tctgcactcg acctgctgag gtccctcagt ccctggtagg cagctttgcc ccgtctgtcc	960
gcccgggtg tgcgggggggt tgacaaggct gttgcgtcag tccaacattt gttgccatat	1020
tttcctgctc tccccaccag ctgtagatct tgggtggcgtg aaactcccgc acctcttcgg	1080
ccagcgcctt gtagaagcgc gtatggcttc gtaccccggc catcaacacg cgtctgcgtt	1140
cgaccaggct gcgcgttctc gcggccatag caaccgacgt acggcgttgc gccctcgccg	1200
gcagcaagaa gccacggaag tccgcccggga gcagaaaatg cccacgctac tgcgggttta	1260
tatagacggg cccacggga tggggaaaac caccaccag caactgctgg tggccctggg	1320
ttcgcgcgac gatatcgtct acgtaccga gccgatgact tactggcggg tgctgggggc	1380
ttccgagaca atcggaaca tctacaccac acaacaccgc ctcgaccagg gtgagatatc	1440
ggccgggggac gcggcgggtg taatgacaag cgcccagata acaatgggca tgccttatgc	1500
cgtgaccgac gccgttctgg ctctcatat cgggggggag gctgggagct cacatgcccc	1560

gcccccgcc	ctcaccctca	tcttcgaccg	ccatcccatc	gccgccctcc	tgtgctaccc	1620
ggccgcgcgg	taccttatgg	gcagcatgac	ccccaggcc	gtgctggcgt	tcgtggccct	1680
catcccgccg	accttgcccc	gcaccaacat	cgtgcttggg	gcccttccgg	aggacagaca	1740
catcgaccgc	ctggccaaac	gccagcgccc	cggcgagcgg	ctggacctgg	ctatgctggc	1800
tgcgattcgc	cgcgtttacg	ggctacttgc	caatacgggtg	cggtatctgc	agtgcggcgg	1860
gtcgtggcgg	gaggactggg	gacagctttc	ggggacggcc	gtgccgcccc	agggtgccga	1920
gccccagagc	aacgcggggc	cacgacccca	tatcggggac	acgttattta	ccctgtttcg	1980
gggccccgag	ttgctggccc	ccaacggcga	cctgtataac	gtgtttgcct	gggccttgga	2040
cgtcttggcc	aaacgcctcc	gttccatgca	cgtctttatc	ctggattacg	accaatcgcc	2100
cgccggctgc	cgggacgccc	tgctgcaact	tacctccggg	atgggtccaga	cccacgtcac	2160
cacccccggc	tccataaccga	cgatatgcga	cctggcgcgc	acgtttgccc	gggagatggg	2220
ggaggctaac	tgaaacacgg	aaggagacaa	taccggaagg	aaccgcgct	atccggatcc	2280
acttaacgtt	actgaaatca	tcaaacagct	tgacgaatct	ggatataaga	tcgttggtgt	2340
cgatgtcagc	tccggagttg	agacaaatgg	tgttcaggat	ctcgataaga	tacgttcatt	2400
tgtccaagca	gcaaagagtg	ccttctagtg	atttaatagc	tccatgtcaa	caagaataaa	2460
acgcgttttc	gggtttacct	cttccagata	cagctcatct	gcaatgcatt	aatgcattga	2520
ctgcaaccta	gtaacgcctt	caggctccgg	cgaagagaag	aatagcttag	cagagctatt	2580
ttcatTTTTcg	ggagacgaga	tcaagcagat	caacggtcgt	caagagacct	acgagactga	2640
ggaatccgct	cttgggtcca	cgcgactata	tatttgtctc	taattgtact	ttgacatgct	2700
cctcttcttt	actctgatag	cttgactatg	aaaattccgt	caccagccct	gggttcgcaa	2760
agataattgc	atgtttcttc	cttgaactct	caagcctaca	ggacacacat	tcatcgtagg	2820
tataaacctc	gaaatcattc	ctactaagat	ggtataacaat	agtaaccatg	catggttgcc	2880
tagtgaatgc	tccgtaacac	ccaatacgcc	ggccgaaact	tttttacaac	tctcctatga	2940
gtcgtttacc	cagaatgcac	aggtacactt	gtttagaggt	aatccttctt	tctagaagtc	3000
ctcgtgtact	gtgtaagcgc	ccactccaca	tctccactcg	acctgcaggc	atgcaagctt	3060
ggcgtaatca	tggtcatagc	tgtttcctgt	gtgaaattgt	tatccgctca	caattccaca	3120
caacatacga	gccggaagca	taaagtgtaa	agcctgggggt	gcctaataag	tgagctaact	3180
cacattaatt	gcgttgcgct	cactgcccgc	tttccagtcg	ggaaacctgt	cgtgccagag	3240

cggccgctct gcattaatga atcggccaac gcgcggggag aggcggtttg cgtattgggc	3300
gctcttccgc ttcctcgctc actgactcgc tgcgctcggc cggtcggctg cggcgagcgg	3360
tatcagctca ctcaaaggcg gtaatacggc tatccacaga atcaggggat aacgcaggaa	3420
agaacatgtg agcaaaaggc cagcaaaagg ccaggaaccg taaaaaggcc gcgttgctgg	3480
cgtttttcca taggctccgc cccctgacg agcatcaca aaatcgacgc tcaagtcaga	3540
ggtggcgaaa cccgacagga ctataaagat accaggcgtt tccccctgga agctccctcg	3600
tgcgctctcc tgttccgacc ctgccgctta ccgataacct gtccgccttt ctcccttcgg	3660
gaagcgtggc gctttctcat agctcacgct gtaggtatct cagttcggtg taggtcgttc	3720
gctccaagct gggctgtgtg cacgaacccc ccgttcagcc cgaccgctgc gccttatccg	3780
gtaactatcg tcttgagtcc aaccggtaa gacacgactt atcgccactg gcagcagcca	3840
ctggtaacag gattagcaga gcgaggtatg taggcgggtgc tacagagttc ttgaagtggc	3900
ggcctaacta cggctacact agaaggacag tatttggtat ctgcgctctg ctgaagccag	3960
ttaccttcgg aaaaagagtt ggtagctctt gatccggcaa acaaaccacc gctggtagcg	4020
gtgggttttt tgtttgcaag cagcagatta cgcgcagaaa aaaaggatct caagaagatc	4080
ctttgatctt ttctacgggg tctgacgctc agtggaacga aaactcacgt taagggattt	4140
tggtcatgag attatcaaaa aggatcttca cctagatcct tttaaattaa aaatgaagtt	4200
ttaaatcaat ctaaagtata tatgagtaaa cttgggtctga cagttaccaa tgcttaatca	4260
gtgaggcacc tatctcagcg atctgtctat ttcgttcac catagttgcc tgactccccg	4320
tcgtgtagat aactacgata cgggagggct taccatctgg cccagtgct gcaatgatac	4380
cgcgagaccc acgctcaccg gctccagatt tatcagcaat aaaccagcca gccggaagg	4440
ccgagcgcag aagtggcctt gcaactttat ccgcctccat ccagtctatt aattgttgcc	4500
gggaagctag agtaagtagt tcgccagtta atagtttgcg caacgttggt gccattgcta	4560
caggcatcgt ggtgtcacgc tcgtcgtttg gtatggcttc attcagctcc ggttcccaac	4620
gatcaaggcg agttacatga tccccatgt tgtgcaaaaa agcggtagc tccttcggtc	4680
ctccgatcgt tgtcagaagt aagttggccg cagtgttatc actcatgggt atggcagcac	4740
tgcataattc tcttactgtc atgccatccg taagatgctt ttctgtgact ggtgagtact	4800
caaccaagtc attctgagaa tagtgtatgc ggcgaccgag ttgctcttgc ccggcgtcaa	4860
tacgggataa taccgcgcca catagcagaa ctttaaaagt gctcatcatt ggaaaacgtt	4920
cttcggggcg aaaactctca aggatcttac cgctgttgag atccagttcg atgtaacca	4980

ctcgtgcacc caactgatct tcagcatctt ttactttcac cagcgtttct gggtgagcaa	5040
aaacaggaag gcaaaatgcc gcaaaaaagg gaataagggc gacacggaaa tggtgaatac	5100
tcatactctt cttttttcaa tattattgaa gcatttatca gggttattgt ctcatgagcg	5160
gatacatatt tgaatgtatt tagaaaaata aacaaatagg gggtccgcgc acatttcccc	5220
gaaaagtgcc acctgacgtc taagaaacca ttattatcat gacattaacc tataaaaaata	5280
ggcgtatcac gaggcccttt cgtctcgcgc gtttcgggtga tgacggtgaa aacctctgac	5340
acatgcagct cccggagacg gtcacagctt gtctgtaagc ggatgccggg agcagacaag	5400
cccgtcaggg cgcgtcagcg ggtgttggcg ggtgtcgggg ctggcttaac tatgcggcat	5460
cagagcagat tgtactgaga gtgcaccata tcgacgtctt cccttatgcg actcctgcat	5520
taggaagcag ccagtagta ggttgaggcc gttgagcacc gccgccgcaa ggaatggtgc	5580
atgcaaggag atggcgccca acagtcccc ggccacgggg cctgccacca taccacgcc	5640
gaaacaagcg ctcatgagcc cgaagtggcg agcccgatct tccccatcgg tgatgtcggc	5700
gatataggcg ccagcaaccg cacctgtggc gccggtgatg ccggccacga tgcgtccggc	5760
gtagaggatc tggctagcga tgaccctgct gattggttcg ctgaccattt ccggggtgcg	5820
gaacggcggt accagaaact cagaagggtc gtccaaccaa accgactctg acggcagttt	5880
acgagagaga tgatagggtc tgcttcagta agccagatgc tacacaatta ggcttgata	5940
tattgtcggt agaacgcggc tacaattaat acataacctt atgtatcata cacatacgat	6000
ttaggtgaca ctata	6015

<210> 51
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<400> 51
 cgcggtatc ctattgcc

18

<210> 52
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Primer

<400> 52
gccggaaatg ttgtacctac 20

<210> 53
<211> 80
<212> DNA
<213> *Aspergillus oryzae*

<400> 53
atgaccgctt gtcataacctg ccgcaagctt aaaactcggg gcgatcttga tccacgaggg 60
catgcctgcc gccgctgcct 80

<210> 54
<211> 80
<212> DNA
<213> *Aspergillus oryzae*

<400> 54
atgactgctt gccacacctg ccgcaagctt aaaactcggg gcgatcttga tccacgaggg 60
catgcctgcc gccgctgcct 80